

GenCore version 4.5
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ON protein - protein search, using sw model

Run on: June 18, 2001, 15:30:32 ; Search time 23:63 seconds

(without alignments) 658.146 Million cell updates/sec

Title:	US-09-653-755A-4	34	429	17.7	391	1	MUCB_HUMAN
Perfect score:	2427	35	426.5	17.6	393	1	HVC3_HETFR
Sequence:	1 EVOLOQSGPELVKPGASVMT..... RHEGLKKNVYLKKTISRSPGK 454	36	421.5	17.4	451	1	HVCM_HETFR
Scoring table:	BLOSUM62	37	421	17.3	479	1	MUCM_RABIT
	Gapop 10.0 , Gapext 0.5	38	420	17.3	450	1	MUC_CANFA
Searched:	93435 seqs, 34255486 residues	39	417	17.2	457	1	MUC_SUNMB
Total number of hits satisfying chosen parameters:	93435	40	416.5	17.2	140	1	HV02_MOUSE
Minimum DB seq length: 0		41	416	17.1	137	1	HV11_MOUSE
Maximum DB seq length: 200000000		42	405	16.7	117	1	HV14_MOUSE
Post-processing: Minimum Match 0%		43	402.5	16.6	353	1	ALCI_GORGO
Maximum Match 100%		44	401	16.5	120	1	HV50_MOUSE
Listing first 45 summaries		45	396.5	16.3	138	1	HV48_MOUSE
Database:	SwissProt_39:*						ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	1802	74.2	336	1 GCB_MOUSE
2	1802	74.0	405	1 GCB_MOUSE
3	1419	58.5	330	1 GCAA_MOUSE
4	1414	58.3	399	1 GCAM_MOUSE
5	1385	57.1	335	1 GCAB_MOUSE
6	1326	54.7	333	1 GCB_RAT
7	1202	49.5	329	1 GCC_RAT
8	1170	48.2	329	1 GCB_MOUSE
9	1159	47.8	398	1 GCB_MOUSE
10	1150	47.4	324	1 GC1_MOUSE
11	1145	47.2	393	1 GC1_MOUSE
12	1112	45.8	326	1 GCL_RAT
13	1100	45.3	322	1 GCA_RAT
14	1087	44.8	330	1 GC1_HUMAN
15	1080	44.5	323	1 GCB_RABBIT
16	1080	44.5	329	1 GCB_CAVPO
17	1059	43.6	326	1 GC2_HUMAN
18	1054	43.4	327	1 GC4_HUMAN
19	776.5	32.0	290	1 GCB_HUMAN
20	478	19.7	454	1 MUC_HUMAN
21	477.5	19.7	429	1 EPC_RAT
22	474	19.5	421	1 EPC_MOUSE
23	473	19.5	428	1 EPC_HUMAN
24	462	19.0	118	1 HV51_MOUSE
25	457.5	18.9	117	1 HV12_MOUSE
26	457.5	18.9	117	1 HV13_MOUSE
27	443.5	18.3	438	1 HV22_HETFR
28	436.5	18.0	370	1 HV21_HETFR
29	436.5	17.8	438	1 HVCS_HETER
30	431	17.8	139	1 HV07_MOUSE
31	431	17.8	458	1 MUC_RABIT
32	430.5	17.7	120	1 HV03_MOUSE
33	429.5	17.7		
1	136			
1	136			
1	HV15_MOUSE			

RESULT 1	DESCRIPTION	SEQUENCE FROM N.A. (A ALLELE)	SEQUENCE FROM N.A. (B ALLELE)	SEQUENCE FROM N.A. (C ALLELE)	SEQUENCE FROM N.A. (D ALLELE)	SEQUENCE FROM N.A. (E ALLELE)	SEQUENCE FROM N.A. (F ALLELE)	SEQUENCE FROM N.A. (G ALLELE)	SEQUENCE FROM N.A. (H ALLELE)	SEQUENCE FROM N.A. (I ALLELE)	SEQUENCE FROM N.A. (J ALLELE)	SEQUENCE FROM N.A. (K ALLELE)	SEQUENCE FROM N.A. (L ALLELE)	SEQUENCE FROM N.A. (M ALLELE)	SEQUENCE FROM N.A. (N ALLELE)	SEQUENCE FROM N.A. (O ALLELE)	SEQUENCE FROM N.A. (P ALLELE)	SEQUENCE FROM N.A. (Q ALLELE)	SEQUENCE FROM N.A. (R ALLELE)	SEQUENCE FROM N.A. (S ALLELE)	SEQUENCE FROM N.A. (T ALLELE)	SEQUENCE FROM N.A. (U ALLELE)	SEQUENCE FROM N.A. (V ALLELE)	SEQUENCE FROM N.A. (W ALLELE)	SEQUENCE FROM N.A. (X ALLELE)	SEQUENCE FROM N.A. (Y ALLELE)	SEQUENCE FROM N.A. (Z ALLELE)											
GCB_MOUSE	STANDARD;																																					
P01866		AC																																				
			DT	21-JUL-1986 (Rel. 01, Created)																																		
				DT	21-JUL-1986 (Rel. 01, last sequence update)																																	
					DT	01-OCT-2000 (Rel. 40, last annotation update)																																
						DE	IG GAMMA-2B CHAIN C REGION.																															
						OS	Mus musculus (Mouse).																															
						OC	Bukiryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muris.																															
						OX	NCBI_TAXID=10090;																															
						RN	Nature 283:786-789(1980).																															
						RP	SEQUENCE FROM N.A. (A ALLELE).																															
						RX	MEDLINE-80120716; PubMed=6766534;																															
						RA	Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.,																															
						RT	"Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from newborn mouse DNA."																															
						RL	Nature 283:786-789(1980).																															
						RT	SEQUENCE FROM N.A. (B ALLELE).																															
						RX	MEDLINE-80081501; PubMed=117548;																															
						RA	Tucker P.W., Marcus K.B., Sliglton J.L., Blattner F.R.,																															
						RT	"Structure of the constant and 3' untranslated regions of the murine gamma 2b heavy chain messenger RNA."																															
						RL	Science 206:1299-1303(1979).																															
						RT	SEQUENCE FROM N.A. (C ALLELE).																															
						RX	MEDLINE-80081502; PubMed=117549;																															
						RA	Tucker P.W., Marcus K.B., Newell N., Richards J., Blattner F.R.,																															
						RT	"Sequence of the cloned gene for the constant region of murine gamma 2b immunoglobulin heavy chain."																															
						RL	Science 206:1303-1306(1979).																															
						RT	SEQUENCE FROM N.A. (D ALLELE).																															
						RX	MEDLINE-8217303; PubMed=6803173;																															
						RA	OLO R., Rougon F.,																															
						RT	"Mouse immunoglobulin allotypes: post-duplication divergence of gamma 2a and gamma 2b chain genes."																															
						RL	Nature 296:761-763(1982).																															
						RT	[5]																															
						RP	CARBOHYDRATE-LINKAGE SITE THR-105.																															
						RX	MEDLINE-9421639; PubMed=7512967.																															
						RA	Kim H., Yamaguchi Y., Matsuda C., Yamamoto K.,																															
						RA	Irimura T., Takahashi N., Kato K., Arata Y.,																															
						RT	"O-glycosylation in hinge region of mouse immunoglobulin G2b."																															
						RL	J. Biol. Chem. 269:12345-12350(1994).																															
						CC	-1- MODIFIED WITH 2 STERIC ACID RESIDUES.																															
						CC	MUC-2																															
						CC	heterodontu																															
						CC	heterodontu																															
						CC	-1- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.																															
						CC	CC																															
						CC	-1- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN																															

DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 150 210
 FT DISULFID 256 314 O-LINKED (GALNAC).
 FT CARBOHYD 105 105 REMOVED POST-TRANSLATIONALLY (PROBABLE).
 FT MOD_RES 336 336 Q -> R (IN B ALLELE).
 FT VARIANT 163 163 T -> A (IN B ALLELE).
 FT VARIANT 194 194 N -> D (IN B ALLELE).
 FT VARIANT 300 300 M -> I (IN B ALLELE).
 FT VARIANT 301 301 L -> S (IN REF. 2 AND 3).
 FT CONFLICT 25 25 S -> P (IN REF. 2 AND 3).
 FT CONFLICT 36 36 I -> T (IN REF. 2 AND 3).
 FT SEQUENCE 239 336 AA; 36658 MW; 7d879662607c356e CRC64;

Query Match 74.2%; Score 1802; DB 1; Length 336;
 Best Local Similarity 100.0%; Pred. No. 1.3e-118; Matches 336; Conservativeness 0; Mismatches 0; Indels 0; gaps 0; CC
 CC

Qy 119 AKTTPPSVYPLAPGGDTGSSVTGLVKGYFPSSVTWNSSHTFPALSG 178
 Db 1 AKTTPPSVYPLAPGGDTGSSVTGLVKGYFPSSVTWNSSHTFPALSG 60

Qy 179 PNLEGGPSVTFPPNPKDVLMSLTPKVKTCVWVVDYSEDDPDVQISWVNNVVEHTAQQT 298
 Db 61 LYTMSSSVTPSSTPSQVTCSVAHASSHTVDKLLEPSPGPISTINPCPPCKBCHKCPA 120

Qy 239 PNLEGGPSVTFPPNPKDVLMSLTPKVKTCVWVVDYSEDDPDVQISWVNNVVEHTAQQT 298
 Db 121 PNLEGGPSVTFPPNPKDVLMSLTPKVKTCVWVVDYSEDDPDVQISWVNNVVEHTAQQT 180

Qy 299 HREDYNSTRVSTLPIQHODWMSKEFKCKVNNKDLPSPTERTISKIGLVRAPQVYL 358
 Db 181 HREDYNSTRVSTLPIQHODWMSKEFKCKVNNKDLPSPTERTISKIGLVRAPQVYL 240

Qy 359 PPAEQLSRKDVSLLCLVWGFNPQDISVETWSNGHTEENYKDTAPVLDSDGSYFIYSKLN 418
 Db 241 PPAEQLSRKDVSLLCLVWGFNPQDISVETWSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300

Qy 419 MKTSWKEKTSFSCNVRHEGLKNYVKKTISRSPK 454
 Db 301 MKTSWKEKTSFSCNVRHEGLKNYVKKTISRSPK 336

RESULT 2

GCBM_MOUSE STANDARD; PRT; 405 AA.

AC GCBM_MOUSE 1
 AC P01867; 21-JUL-1996 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2B CHAIN C REGION, MEMBRANE-BOUND FORM.
 OS MUS musculus (mouse).
 EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OC [NCBI-TAXID=10090]; [1]
 RP SEQUENCE OF 335-405 FROM N.A. RX MEDLINE=8222210; RX PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Minata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RT Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 RN [2]
 RP SEQUENCE OF 335-378 FROM N.A.

Query Match 74.0%; Score 1797; DB 1; Length 405;
 Best Local Similarity 100.0%; Pred. No. 3.6e-118; Matches 335; Conservativeness 0; Mismatches 0; Indels 0; gaps 0; CC
 CC

Qy 119 AKTTPPSVYPLAPGGDTGSSVTGLVKGYFPSSVTWNSSHTFPALSG 178
 Db 1 AKTTPPSVYPLAPGGDTGSSVTGLVKGYFPSSVTWNSSHTFPALSG 60

Qy 179 PNLEGGPSVTFPPNPKDVLMSLTPKVKTCVWVVDYSEDDPDVQISWVNNVVEHTAQQT 298
 Db 121 PNLEGGPSVTFPPNPKDVLMSLTPKVKTCVWVVDYSEDDPDVQISWVNNVVEHTAQQT 180

Qy 299 HREDYNSTRVSTLPIQHODWMSKEFKCKVNNKDLPSPTERTISKIGLVRAPQVYL 358
 Db 61 LYTMSSSVTPSSTPSQVTCSVAHASSHTVDKLLEPSPGPISTINPCPPCKBCHKCPA 120

Qy 239 PNLEGGPSVTFPPNPKDVLMSLTPKVKTCVWVVDYSEDDPDVQISWVNNVVEHTAQQT 298
 Db 181 HREDYNSTRVSTLPIQHODWMSKEFKCKVNNKDLPSPTERTISKIGLVRAPQVYL 240

Qy 359 PPAEQLSRKDVSLLCLVWGFNPQDISVETWSNGHTEENYKDTAPVLDSDGSYFIYSKLN 418
 Db 241 PPAEQLSRKDVSLLCLVWGFNPQDISVETWSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300

QY	419	MKTWKWEKTDTSFSCNVRHGLKNYLYKKTTSRSG	453	FT	DISUFID	27	82	INTERCHAIN (WITH A HEAVY CHAIN).
Db	301	MKTWKWEKTDTSFSCNVRHGLKNYLYKKTTSRSG	335	FT	DISUFID	107	107	INTERCHAIN (WITH A HEAVY CHAIN).
RESULT	3			FT	DISUFID	110	110	INTERCHAIN (WITH A HEAVY CHAIN).
GCAL_MOUSE				FT	DISUFID	112	112	INTERCHAIN (WITH A HEAVY CHAIN).
ID	GCAA_MOUSE	STANDARD;	PRT;	FT	DISUFID	144	204	
AC	P01863;			FT	DISUFID	250	308	
DT	21-JUL-1986 (Rel. 01, Created)			FT	DISUFID	330	330	REMOVED POST-TRANSLATIONALLY.
DT	21-JUL-1986 (Rel. 01, last sequence update)			FT	DISUFID	330 AA;	36389 MW;	BB4361c5445a6864 CRC64;
DT	30-MAY-2000 (Rel. 39, Last annotation update)			FT	MOD_RES	330 AA;	36389 MW;	BB4361c5445a6864 CRC64;
DE	IG GAMMA-2A CHAIN C REGION, A ALLELE.			SQ	SEQUENCE	330 AA;	36389 MW;	BB4361c5445a6864 CRC64;
OS								
OC	Mus musculus (Mouse)			Query	Match	58.5 %;	Score 1419;	DB 1; Length 330;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			DB	Best Local Similarity	78.8 %;	Pred. No. 5. 9e-92;	Indels 6; Gaps 2;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			DB	Matches	264;	Conservative 30;	Mismatches 36;
OX				DB	1	AKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPVWTFNWSGLSSGVHTFPVQSD	178	
RN	[1]			Db	119	AKTPPSVYPLAPCQGDTGSSVTLGCLVKGYFPEPVWTFNWSGLSSGVHTFPALOSG	178	
RP	SEQUENCE FROM N.A.			Db	61	LYTLLSSVYTWSWPSQSTCNAHPASSTKVDKKIPRGRG-TIKCPC---KCPA	114	
RX	MEDLINE-81070554; PubMed=6777755;			Db	239	PNLGGPSVTFPPNIKDMISLTPKVCVWVVDSEDDPQDQISWFTVNNVFTAOFT	298	
RA	Sikorav J.-L., Aufray C., Rougeon F.;			Db	115	PNLGGPSVTFPPNIKDMISLSPVIVCWWVVDSEDDPQDQISWFTVNNVFTAOFT	174	
RT	"Structure of the constant and 3' untranslated regions of the murine			Db	299	HREDYNSTRLVVAWSLPIQHQDWMSGKEPKVNNKDLSPPIERISKKGVLVAPQVIL	358	
RT	Balb/c gamma 2a heavy chain messenger RNA.;"			Db	175	HREDYNSTRLVVAWSLPIQHQDWMSGKEPKVNNKDLSPPIERISKKGVLVAPQVIL	358	
RL	Nucleic Acids Res. 8:3143-3155(1980).			Db	359	PPPABQLSRKDVSLTCVVGPNPGDISVETNSGTCVTEENYKUTAPVLDSDGSYFIYSLN	418	
RN	[3]			Db	235	PPPEBEMTKQVITCMYDFMPDIDVWETWNNGKTELYKNTEPVLDSDGSYFMSKL	294	
RP	SEQUENCE FROM N.A.			Db	419	MKTWKWEKTDTSFSCNVRHGLKNYLYKKTTSRSG	454	
RX	MEDLINE-81223894; PubMed=6787604;			Db	295	VEKKVVERNSYSCSVVHGLHNHHTKSSFRTPK	330	
RA	Ollé R., Aufray C., Marcham C., Rougeon F.;							
RT	"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic							
RT	family.";							
RL	Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).							
RN	[4]							
RP	MYELOMA PROTEIN MOPC 173.							
RX	MEDLINE-74175517; PubMed=4831970;							
RA	Bourgois A., Fougerousse M., Rocca-Serra J.;							
RT	"Determination of the primary structure of a mouse IgG2a immunoglobulin: amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.;"							
RT	Eur. J. Biochem. 43:423-435(1974).							
RL	[5]							
RN	DISULFIDE BONDS.							
RX	MEDLINE-73056887; PubMed=4565406;							
RA	de Preval C., Fougerousse M.;							
RT	"Determination of the primary structure of the disulfide bridges.;"							
RT	Eur. J. Biochem. 30:452-462(1972).							
CC	-----							
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CC	-----							
EMBL: V00798; CAA24178.1; -.								
DR	PIR: A02152; G2MSA.							
DR	InterPro: IPR00495; -.							
DR	InterPro: IPR003000; -.							
DR	Pfam: PF00047; 1;							
DR	PROSITE: PS00290; IG_MHC; 1.							
KW	Immunoglobulin domain; Immunoglobulin C region.							
FT	NON_TER 1							
FT	DISULFID 15							
FT	INTERCHAIN (WITH A LIGHT CHAIN) 15							
CC	-----							
CC	IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF THE A ALLELE.							
CC	-----							
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CC	-----							

CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RT	IgG2aa and IgG2ab alleles of the mouse. ";
CC		RL	Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499 (1981).
CC		RN	[2]
DR		RP	SEQUENCE.
DR		RX	MEDLINE=8203777; PUBMED=6794027;
DR		RA	Dognin M.J.; Lauwereys M.; Strosberg A.D.;
DR		RT	"Multiple amino acid substitutions between murine gamma 2a heavy chain Fc regions of Ig1a and Ig1b allotypic forms. ";
DR		RL	Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035 (1981).
DR		CC	-1- MISCELLANEOUS: THE SEQUENCE DIFERS FROM THAT OF THE A ALLELE, FROM BALB/C MICE, AT 15% OF THE POSITIONS.
KW	Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.	CC	
FT	NON_TER 1 1	CC	
FT	DISULFD 15 15	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
FT	DISULFD 27 82	CC	CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
FT	DISULFD 107 107	CC	
FT	DISULFD 110 110	CC	
FT	DISULFD 112 112	CC	
FT	DISULFD 144 204	CC	
FT	DISULFD 250 308	CC	
FT	TRANSMEM 346 363	CC	
FT	DOMAIN 364 399	CC	
FT	CARBOHYD 180 180	CC	
SO	SEQUENCE 399 AA; 44020 MW; 4C38138PRAED3FF0 CRC64;	CC	
Query Match 58.3%; Score 1414; DB 1; Length 399; Best Local Similarity 78.5%; Pred. No. 1.7e-91; Matches 263; Conservative 30; Mismatches 36; Indels 6; Gaps 2; Non_TER 1 1	FT	DR	EMBL; J00479; -; NOT_ANNOTATED_CDS.
Db 1 AKTTAPSVPVPLAPGCDDTGSVTGLCKLVKGYPESVTWNSGSSSVTFFPALQSG 60	DR	DR	PIR; A02153; GNSAB.
Oy 179 LYTMSSSVTWSSTWSQTVCSVARPASSTVDKKLEPSGPPISTINPCPCKECHKCPA 238	DR	DR	InterPro; IPR000495; -.
Db 61 LYTLSSSVTWSSTWSQSTVCKVNNKDLPSPIERTSKIKLVRAQVYL 178	DR	DR	PROSITE; PS00290; Ig_MHC; 1.
Oy 239 PNLEGGPSVFLPPNPKDVLMSLPLPKVTCWVDSSEDDPDVQISMFWNNNEVHTAQQT 298	DR	DR	EMBL; J00479; -; NOT_ANNOTATED_CDS.
Db 115 PNLLGQSPVLFPPKIKDVMLISLSPVTCWVDSSEDDPDVQISMFWNNNEVHTAQQT 174	DR	DR	PIR; A02153; GNSAB.
Oy 299 HREDYNSTIRVSTLPIQHODWMSKEFKCKVNNKDLPSPIERTSKIKLVRAQVYL 358	DR	DR	InterPro; IPR000506; -.
Db 175 HREDYNSTIRVSTLPIQHODWMSKEFKCKVNNKDLPSPIERTSKIKLVRAQVYL 234	DR	DR	PROSITE; PS00290; Ig_MHC; 1.
Oy 359 PPPAEDLSRKVSLTCLWVGPNPGDISVEMTSNGHENEENKTATPLDSGSYIYSKLN 418	DR	DR	EMBL; J00479; -; NOT_ANNOTATED_CDS.
Db 235 PPPEERMTKQVTLCTMVTDFMPEDIVVETNNGKTELNYKNTEPVLDSGSYIYSKL 294	DR	DR	PIR; A02153; GNSAB.
Oy 419 MKTSKWEKTDSSFCNVRHEGKKNYKVKTTSRSPG 453	DR	DR	InterPro; IPR000495; -.
Db 295 VEKKVNRVNSCSVYHEGLNLHHTKSFRTPG 329	DR	DR	PROSITE; PS00290; Ig_MHC; 1.
RESULT 5	Qy 419 MKTSKWEKTDSSFCNVRHEGKKNYKVKTTSRSPG 454	DR	EMBL; J00479; -; NOT_ANNOTATED_CDS.
GCAB_MOUSE	AC 335 AA.	DR	PIR; A02153; GNSAB.
ID GCAB_MOUSE	STANDARD; PRT;	DR	InterPro; IPR000506; -.
DT 21-JUL-1986 (Rel. 01, Last sequence update)	DR	DR	PROSITE; PS00290; Ig_MHC; 1.
DT 15-JUL-1999 (Rel. 3B, Last annotation update)	DR	DR	EMBL; J00479; -; NOT_ANNOTATED_CDS.
DE IG_GAMMA-2A_CHAIN_C_REGION, B ALLELE.	DR	DR	PIR; A02153; GNSAB.
OS Mus musculus (Mouse)	OC	DR	InterPro; IPR000495; -.
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. RN NCBI_TaxID=10090; [1]	OX	DR	PROSITE; PS00290; Ig_MHC; 1.
SEQUENCE FROM N.A.	RP	DR	EMBL; J00479; -; NOT_ANNOTATED_CDS.
RC STRAIN=C57BL/6;	RC	DR	PIR; A02153; GNSAB.
RX MEDLINE=82037861; PubMed=6170065;	RX	DR	InterPro; IPR000495; -.
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.; RN NCBI_TaxID=10116; [1]	RA	DR	PROSITE; PS00290; Ig_MHC; 1.
"Multiple differences between the nucleic acid sequences of the	RN	DR	EMBL; J00479; -; NOT_ANNOTATED_CDS.

RP	SEQUENCE FROM N.A.
RX	MIDDLEN-8932738; PubMed=3149946;
RA	Brueggemann M.;
RT	"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL	Gene 74:473-482(1988).
DR	PS0018; PS0018;
DR	InterPro; IPR000495; -;
DR	InterPro; IPR003006; -;
PFam	PF00047; ig; 3;
DR	PROSITE; PS00290; IG_MHC; 1;
KW	Immunoglobulin domain; Immunoglobulin C region.
FT	NON_TER 1 1
FT	DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID 27 80 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 106 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 147 207
FT	DISULFID 253 311
FT	DISULFID 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;
SQ	SEQUENCE
Query Match	54.7%; Score 1326.5; DB 1; Length 333;
Best Local Similarity	73.6%; Pred. No. 1.6e-85;
Matches	248; Conservative 34; Mismatches 50; Indels 5; Gaps 3;
Qy	119 AKTPPPSVVPLAPGCGDTGSSVTLGKGKFPESTVVTWNNSLSSSVHFTPALQSG 178
Db	1 AQTAPSVPVPLAPGCGDTTSSATVLGKGKFPEPVTVWNSSGALSDVHTPAVQSG 60
Qy	179 LYTMSSSVTPSSWTQPTVCSVHAPASSTVDKKLE-PSPCPISTINPCPCKECKRCP 237
Db	61 LYTLSSVT - SSIWPSQTVTCVNAVAHBASTKVDKVYRNGG - HKCPICPCTCHKCP 116
Qy	238 APNLEGSVPSVLFPPNPKDVLIMSLTPTKVCVWVDSSEDPDPOVQISWVNNTVHQTQ 297
Db	117 VPELLGGPSVFTPPKPKDILLISONAKVTCVWVDSSEEDPDQVQISWVNNTVHQTQ 176
Qy	298 THREDDNSTIRVSLPIQHQDWMSGKEFKCKVNNKDLSPPIERTISKIGLVRAPOVYI 357
Db	177 PREEQYNSTFRVSLPIQHQDWMSGKEFKCKVNNKALSPPIEKTSKPKGLVRAPOVYI 236
Qy	358 LPPPAEQLRSKVLCLVGVGNPGDLSVWNTSNGHTEENYKDTAPVLDSDSYFISKL 417
Db	237 MGPPTQTELTQTVSLTCLTSGFLPNUDIGVWEWTSNGHTEENYKNTPEVMDSDGSPFMSKL 296
Qy	418 NMKTSKWEKTDTSFCNVRHGKKNYVKKTISRSQPK 454
Db	297 NVERSRSRAPFVCSVVHGLHNHRVEKSTSRPPGK 333
RESULT	7
GCC_RAT	STANDARD; PRT; 329 AA.
AC	P20762;
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG_GAMMA-2C CHAIN C REGION.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=88166903; PubMed=3127222;
RA	Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT	"Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
RL	Eur. J. Immunol. 18:317-319(1988).
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CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Use by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; X07189; CAA30169.1; -;
CC	PIR; S00847; S00847;
CC	InterPro; IPR00495; -;
CC	InterPro; IPR003006; -;
CC	Pfam; PF00047; ig; 3;
CC	PROSITE; PS00290; IG_MHC; 1;
CC	Immunoglobulin domain; Immunoglobulin C region.
DR	NON_TER 1 1
DR	DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
DR	DISULFID 27 80 INTERCHAIN (WITH A HEAVY CHAIN).
DR	DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
DR	DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
DR	DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
DR	DISULFID 147 207
DR	DISULFID 253 311
DR	DISULFID 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;
DR	SEQUENCE
Query Match	49.5%; Score 1202.5; DB 1; Length 329;
Best Local Similarity	68.2%; Pred. No. 7e-77;
Matches	239; Conservative 35; Mismatches 65; Indels 7; Gaps 4;
Qy	119 AKTPPPSVVPLAPGCGDTGSSVTLGKGKFPESTVVTWNNSLSSSVHFTPALQSG 178
Db	1 AQTAPSVPVPLAPGCGDTTSSATVLGKGKFPEPVTVWNSSGALSDVHTPAVQSG 60
Qy	179 LYTMSSSVTPSSWTQPTVCSVHAPASSTVDKKLE-PSPCPISTINPCPCKECKRCP 237
Db	61 LYTLSSVT - SSIWPSQTVTCVNAVAHBASTKVDKVYRNGG - HKCPICPCTCHKCP 116
Qy	238 APNLEGSVPSVLFPPNPKDVLIMSLTPTKVCVWVDSSEDPDPOVQISWVNNTVHQTQ 297
Db	117 VPELLGGPSVFTPPKPKDILLISONAKVTCVWVDSSEEDPDQVQISWVNNTVHQTQ 176
Qy	298 THREDDNSTIRVSLPIQHQDWMSGKEFKCKVNNKDLSPPIERTISKIGLVRAPOVYI 357
Db	177 PREEQYNSTFRVSLPIQHQDWMSGKEFKCKVNNKALSPPIEKTSKPKGLVRAPOVYI 236
Qy	358 LPPPAEQLRSKVLCLVGVGNPGDLSVWNTSNGHTEENYKDTAPVLDSDSYFISKL 417
Db	237 MGPPTQTELTQTVSLTCLTSGFLPNUDIGVWEWTSNGHTEENYKNTPEVMDSDGSPFMSKL 296
Qy	418 NMKTSKWEKTDTSFCNVRHGKKNYVKKTISRSQPK 454
Db	297 NVERSRSRAPFVCSVVHGLHNHRVEKSTSRPPGK 333
RESULT	7
GCC_RAT	STANDARD; PRT; 329 AA.
AC	P20762;
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG_GAMMA-2C CHAIN C REGION.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=88166903; PubMed=3127222;
RA	Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT	"Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
RL	Eur. J. Immunol. 18:317-319(1988).
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; X07189; CAA30169.1; -;
CC	PIR; S00847; S00847;
CC	InterPro; IPR00495; -;
CC	InterPro; IPR003006; -;
CC	Pfam; PF00047; ig; 3;
CC	PROSITE; PS00290; IG_MHC; 1;
CC	Immunoglobulin domain; Immunoglobulin C region.
DR	NON_TER 1 1
DR	DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
DR	DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
DR	DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
DR	DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
DR	DISULFID 143 203
DR	DISULFID 249 307
DR	SEQUENCE
Query Match	49.5%; Score 1202.5; DB 1; Length 329;
Best Local Similarity	68.2%; Pred. No. 7e-77;
Matches	239; Conservative 35; Mismatches 65; Indels 7; Gaps 4;
Qy	119 AKTPPPSVVPLAPGCGDTGSSVTLGKGKFPESTVVTWNNSLSSSVHFTPALQSG 178
Db	1 AQTAPSVPVPLAPGCGDTTSSATVLGKGKFPEPVTVWNSSGALSDVHTPAVQSG 60
Qy	179 LYTMSSSVTPSSWTQPTVCSVHAPASSTVDKKLE-PSPCPISTINPCPCKECKRCP 237
Db	61 LYTLSSVT - SSIWPSQTVTCVNAVAHBASTKVDKVYRNGG - HKCPICPCTCHKCP 116
Qy	238 APNLEGSVPSVLFPPNPKDVLIMSLTPTKVCVWVDSSEDPDPOVQISWVNNTVHQTQ 297
Db	117 VPELLGGPSVFTPPKPKDILLISONAKVTCVWVDSSEEDPDQVQISWVNNTVHQTQ 176
Qy	298 THREDDNSTIRVSLPIQHQDWMSGKEFKCKVNNKDLSPPIERTISKIGLVRAPOVYI 357
Db	177 PREEQYNSTFRVSLPIQHQDWMSGKEFKCKVNNKALSPPIEKTSKPKGLVRAPOVYI 236
Qy	358 LPPPAEQLRSKVLCLVGVGNPGDLSVWNTSNGHTEENYKDTAPVLDSDSYFISKL 417
Db	237 MGPPTQTELTQTVSLTCLTSGFLPNUDIGVWEWTSNGHTEENYKNTPEVMDSDGSPFMSKL 296
Qy	418 NMKTSKWEKTDTSFCNVRHGKKNYVKKTISRSQPK 454
Db	297 NVERSRSRAPFVCSVVHGLHNHRVEKSTSRPPGK 333
RESULT	8
GC3_MOUSE	STANDARD; PRT; 329 AA.
ID	GC3_MOUSE
AC	P22436;
DT	01-AUG-1991 (Rel. 19, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG_GAMMA-3 CHAIN C REGION, SECRETED FORM.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=88166903; PubMed=3127222;
RA	Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT	"Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
RL	Eur. J. Immunol. 18:317-319(1988).
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; X07189; CAA30169.1; -;
CC	PIR; S00847; S00847;
CC	InterPro; IPR00495; -;
CC	InterPro; IPR003006; -;
CC	Pfam; PF00047; ig; 3;
CC	PROSITE; PS00290; IG_MHC; 1;
CC	Immunoglobulin domain; Immunoglobulin C region.
DR	NON_TER 1 1
DR	DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
DR	DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
DR	DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
DR	DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
DR	DISULFID 143 203
DR	SEQUENCE
Query Match	49.5%; Score 1202.5; DB 1; Length 329;
Best Local Similarity	68.2%; Pred. No. 7e-77;
Matches	239; Conservative 35; Mismatches 65; Indels 7; Gaps 4;
Qy	119 AKTPPPSVVPLAPGCGDTGSSVTLGKGKFPESTVVTWNNSLSSSVHFTPALQSG 178
Db	1 AQTAPSVPVPLAPGCGDTTSSATVLGKGKFPEPVTVWNSSGALSDVHTPAVQSG 60
Qy	179 LYTMSSSVTPSSWTQPTVCSVHAPASSTVDKKLE-PSPCPISTINPCPCKECKRCP 237
Db	61 LYTLSSVT - SSIWPSQTVTCVNAVAHBASTKVDKVYRNGG - HKCPICPCTCHKCP 116
Qy	238 APNLEGSVPSVLFPPNPKDVLIMSLTPTKVCVWVDSSEDPDPOVQISWVNNTVHQTQ 297
Db	117 VPELLGGPSVFTPPKPKDILLISONAKVTCVWVDSSEEDPDQVQISWVNNTVHQTQ 176
Qy	298 THREDDNSTIRVSLPIQHQDWMSGKEFKCKVNNKDLSPPIERTISKIGLVRAPOVYI 357
Db	177 PREEQYNSTFRVSLPIQHQDWMSGKEFKCKVNNKALSPPIEKTSKPKGLVRAPOVYI 236
Qy	358 LPPPAEQLRSKVLCLVGVGNPGDLSVWNTSNGHTEENYKDTAPVLDSDSYFISKL 417
Db	237 MGPPTQTELTQTVSLTCLTSGFLPNUDIGVWEWTSNGHTEENYKNTPEVMDSDGSPFMSKL 296
Qy	418 NMKTSKWEKTDTSFCNVRHGKKNYVKKTISRSQPK 454
Db	297 NVERSRSRAPFVCSVVHGLHNHRVEKSTSRPPGK 333
RESULT	8
GC3_MOUSE	STANDARD; PRT; 329 AA.
ID	GC3_MOUSE
AC	P22436;
DT	01-AUG-1991 (Rel. 19, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG_GAMMA-3 CHAIN C REGION, SECRETED FORM.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=88166903; PubMed=3127222;
RA	Wells J.A., Word C.J., Rimm D., Der-Balani G.P., Martinez H.M.,

RA TUCKER P.W.; Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene.";
 RL EMB0 J. 3:2041-2046(1984).
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; J00451; -, NOT_ANNOTATED_CDS.
 DR PIR; B02156; G3MSC.
 DR InterPro; IPR00095; -.
 DR InterPro; IPR03006; -.
 DR Pfam; PF00047; 1g; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin C region; Glycoprotein; Transmembrane;
 KW Alternative splicing.
 FT NON_TER 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;
 Query Match 48.2%; Score 1170; DB 1; Length 329;
 Best Local Similarity 66.2%; Pred. No. 1.3e-74; Mismatches 74; Indels 6; Gaps 1;
 Matches 221; Conservative 33; MisMatches 74; Index 1;
 QY 121 TTPPSVPLAPGGDDTGSVTIGCLYKGFPESTVTWNSSSLSSVHTPALLQSGLY 180
 DB 2 TTAPSVPVPLVPCSDTSGSVTIGCLYKGFPEPTVWNSYGAISGSGVTVSSVLSQFF 61
 QY 181 TMSSSVTPSSTWSSQTVICNVAHPSKTELRIEPR-----IPKSTPSSCPCP 240
 DB 62 SLSSLVVTPSSWPSQTVICNVAHPSKTELRIEPR-----IPKSTPSSCPCP 115
 QY 241 LEGGSVFLPPNPKDVLMSLTPKVCVWVQYEDPPDQ15WSPFVNNEVHTAQTHR 300
 DB 116 ILGGSPVFLPPKPKDLMISLTPKVCVWVQYEDPPDQ15WSPFVNNEVHTAQTHR 175
 QY 301 EDYNSTIRVSTLQIHOQDMWSGKFKCKVNNKDLPSPIERTISKIGLVRAPQVYILP 360
 DB 176 AQYNSITRVSALPQIHOQDMWSGKFKCKVNNKALPAPERTISKPKGRQTPQWVITP 235
 QY 361 PAEQLSRKDSVSLTCLVWGVNPQSDISVEMTSNGHTEENYKDTAFLVLDSDGSYFLYSKLMK 420
 DB 236 PREOMSKKKVSVLTCLVNFSEASIVEWERNELQDQYKNTPPILDSDGTYFLYSKLMK 295
 QY 421 TSKWEKUDSFSCNVRHEGLKKNYKKTLSRSPGK 454
 DB 296 TDSWLQBLFIFTCSVVHAEHLHNHTQKNLRSRSPGK 329
 SEQUENCE 398 AA; 43929 MW; CTF264B50A41B95 CRC64;
 Query Match 47.8%; Score 1159; DB 1; Length 398;
 Best Local Similarity 66.0%; Pred. No. 9.5e-74; Mismatches 74; Indels 6; Gaps 1;
 Matches 219; Conservative 33; MisMatches 74; Index 1;
 QY 121 TTPPSVPLAPGGDDTGSVTIGCLYKGFPESTVTWNSSSLSSVHTPALLQSGLY 180
 DB 2 TTAPSVPVPLVPCSDTSGSVTIGCLYKGFPEPTVWNSYGAISGSGVTVSSVLSQFF 61
 QY 181 TMSSSVTPSSTWSSQTVICNVAHPSKTELRIEPR-----IPKSTPSSCPCP 240
 DB 62 SLSSLVVTPSSWPSQTVICNVAHPSKTELRIEPR-----IPKSTPSSCPCP 115
 QY 241 LEGGSVFLPPNPKDVLMSLTPKVCVWVQYEDPPDQ15WSPFVNNEVHTAQTHR 300
 DB 116 ILGGSPVFLPPKPKDLMISLTPKVCVWVQYEDPPDQ15WSPFVNNEVHTAQTHR 175
 QY 301 EDYNSTIRVSTLQIHOQDMWSGKFKCKVNNKDLPSPIERTISKIGLVRAPQVYILP 360
 DB 176 AQYNSITRVSALPQIHOQDMWSGKFKCKVNNKALPAPERTISKPKGRQTPQWVITP 235
 QY 361 PAEQLSRKDSVSLTCLVWGVNPQSDISVEMTSNGHTEENYKDTAFLVLDSDGSYFLYSKLMK 420
 DB 236 PREOMSKKKVSVLTCLVNFSEASIVEWERNELQDQYKNTPPILDSDGTYFLYSKLMK 295
 QY 421 TSKWEKUDSFSCNVRHEGLKKNYKKTLSRSPGK 454
 DB 296 TDSWLQBLFIFTCSVVHAEHLHNHTQKNLRSRSPGK 329
 SEQUENCE FROM N.A.
 MEDLINE=8502761; PubMed=6092053;
 RX Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA GCL_MOUSE
 RP RESULT 10
 CC

RP	SEQUENCE OF 323-366 FROM N.A.
RX	MEDLINE=82115295; PubMed=6799207;
RA	Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.
RT	Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains. ";
RL	Cell 26:19-27 (1981).
RN	[4]
RP	SEQUENCE OF 1-44 FROM N.A.
RA	MEDLINE=8222190; PubMed=6283537;
RX	Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT	Immunoglobulin gamma chains. ";
RL	immunoglobulin gamma chains. ";
CC	Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627 (1982).
CC	-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGS CONTAIN TWO mRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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CC	or send an email to license@isb-sib.ch).
CC	EMBL: V00793; CAA24172.1; -.
DR	EMBL: V00793; CAA24174.1; -.
DR	PIR: B02199; GI:MSM.
DR	MGD: MGI:96446; IgH:4.
DR	InterPro: IPR00495; -.
DR	InterPro: IPR003006; -.
DR	Pfam: PF00047; Ig; 3.
DR	PROSITE; PS00250; Ig_MHC; 1.
KW	Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing; transmembrane.
FT	NON_TER 1 1
FT	DOMAIN 1 97 CH1.
FT	DOMAIN 98 110 HINGE.
FT	DOMAIN 111 217 CH2.
FT	DOMAIN 218 324 CH3.
FT	DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 140 200 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 246 304 N-LINKED (GLCNAC. . .).
FT	DISULFID 244 302 CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT	DISULFID 340 357 POTENTIAL.
FT	TRANSEME 358 393 CYTOPLASMIC (POTENTIAL).
SQ	SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;
Query Match	47.2%; Score 1145; DB 1; Length 393;
Best Local Similarity	64.5%; Pred. No. 8.8e-73; Mismatches 62; Indels 12; Gaps 4;
Matches	216; Conservative 45; Mismatches 62; Indels 12; Gaps 4;
Query	119 AKTTPPSVPLAPGGDTGSSVTGCLVKYGFPSVTWNSGSSLSSVHTPALLOG 178
Db	1 AKTTPPSVPLAPGGDTGSSVTGCLVKYGFPSVTWNSGSSLSSVHTPALLOG 60
Query	179 LYTMSSSVTPSSWPSQTVTCVSAHPSSTVVKLKEPLSGP1STINCPCKCKHCPA 238
Db	61 LYTMSSSVTPSSWPSQTVTCVSAHPSSTVVKLKEPLSGP1STINCPCKCKHCPA 113
Query	239 PNLEGGPSVTFPPNPKDMLISLTPKVTWVWDISSEDPDVQISWFWVNVNEVHTAQ 298
Db	61 LYTMSSSVTPSSWPSQTVTCVSAHPSSTVVKLKEPLSGP1STINCPCKCKHCPA 110
Query	239 PNLEGGPSVTFPPNPKDMLISLTPKVTWVWDISSEDPDVQISWFWVNVNEVHTAQ 298
Db	112 PEVS---SVFIFPKPKDVLITLTPKVTWVWDISKDPEVQFSWFVVDVVEVHTAQ 230
Query	299 HREDVNSTIRVSTPLIQHODWMSCREFKCKVNNKDLPSDERTTSIKGLVRAPVYIL 358
Db	169 REEQNSTFRESVSELPIMHQDWNGKEFKCRVNSHAPPAPLEKITSKTKGRKARQVYI 228
Query	359 PPPAROLSKRIVSLSCLVWGFNPQGIVSVENTSNGTTEENYKDTAVLSDGSYTIYSK 418
Db	229 PPPKEOMAKDVKSLATCMTDFPPEPDITVWQWNGQPAENYKNTOPIMNTGSYFVYSKL 288
Query	419 MTKSWKETTSFSCAVRHEKLNKYLKKTISRSPG 453
Db	289 VOKSWEAGHTFTCSVLYHSGLHWHTEKSLSHSPG 323
RESULT	12
GC1_RAT	STANDARD;
ID	GCL_RAT
AC	P20759;
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG GAMMA-1 CHAIN C REGION.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX
RA	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89232738; PubMed=3149946;
RA	Brusegemann M.; -.
RT	"Evolution of the rat immunoglobulin gamma heavy-chain gene family. ";
RL	Gene 74:473-482 (1988).
PIR	PS0017; PS0017.
DR	InterPro; IPR00495; -.
DR	InterPro; IPR003006; -.
DR	Pfam; PF00047; Ig; 3.
DR	PROSITE; PS00290; Ig_MHC; 1.
KW	Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT	NON_TER 1 1 CH1.
FT	DOMAIN 1 97 HINGE.
FT	DOMAIN 98 112 CH2.
FT	DOMAIN 113 219 CH3.
FT	DOMAIN 220 326 CH3.
FT	DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 140 200 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 246 304 N-LINKED (GLCNAC. . .).
FT	DISULFID 246 304 N-LINKED (GLCNAC. . .).
SQ	SEQUENCE 326 AA; 35946 MW; 013BAB45F49B9DA CRC64;
Query Match	45.8%; Score 1112; DB 1; Length 326;
Best Local Similarity	61.9%; Pred. No. 1.4e-70; Mismatches 68; Indels 10; Gaps 3;
Matches	208; Conservative 50; Mismatches 68; Indels 10; Gaps 3;
Query	119 AKTTPPSVPLAPGGDTGSSVTGCLVKYGFPSVTWNSGSSLSSVHTPALLOG 178
Db	1 AKTTPPSVPLAPGGDTGSSVTGCLVKYGFPSVTWNSGSSLSSVHTPALLOG 60
Query	179 LYTMSSSVTPSSWPSQTVTCVSAHPSSTVVKLKEPLSGP1STINCPCKCKHCPA 238
Db	61 LYTMSSSVTPSSWPSQTVTCVSAHPSSTVVKLKEPLSGP1STINCPCKCKHCPA 113
Query	239 PNLEGGPSVTFPPNPKDMLISLTPKVTWVWDISSEDPDVQISWFWVNVNEVHTAQ 358
Db	114 SEVS---SVFIFPKPKDVLITLTPKVTWVWDISKDPEVQFSWFVVDVVEVHTAQ 170
Query	299 HREDYNSTIRVSTPLIQHODWMSCREFKCKVNNKDLPSDERTTSIKGLVRAPVYIL 358
Db	171 PEEQNSTFRESVSELPIMHQDWNGKEFKCRVNSHAPPAPLEKITSKTKGRKARQVYI 230

RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nle), I: Purification and
 RT characterization of the L-, H- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges. ";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=1208100; PubMed=236608;

RA Deisenhofer J.;
 RT "Crystalllographic refinement and atomic models of a human Fc fragment
 and its complex with fragment B of protein A from *Staphylococcus*
 aureus at 2.9- and 2.8-A resolution";

RT Biochemistry 20:2361-2370(1981).

RL -!- MISCELLANEOUS: NLE HAS THE GIM(17) ALLOSTATIC MARKER, 97 K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -!- MISCELLANEOUS: NLE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267/272.

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 CC or send an email to license@ebi.ac.uk).

CC EMBL; J00228; AAC82527.1; ALT-INIT.

DR PIR: A02146; GHIIU.

DR PDB; 1FC1; 15-JUL-92.

DR PDB; 1FC2; 15-JUL-92.

MM: 147100; -.

DR Interpro; IPR00495; -.

DR Interpro; IPR00506; -.

PFAM; PF00047; 19; 3.

DR PROSITE; PS00290; IG_MHC; 2.

DR KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.

FT NON_TER 1 1

FT DOMAIN 1 98 CH1.

FT DOMAIN 99 110 HINGE.

FT DOMAIN 111 223 CH2.

FT DOMAIN 224 330 CH3.

FT DISULFD 27 83 INTERCHAIN (WITH LIGHT CHAIN).

FT DISULFD 103 103 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFD 109 109 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFD 112 112 INTERCHAIN (WITH HEAVY CHAIN).

FT DISULFD 144 204 DISULFD

FT DISULFD 250 308 N-LINKED (GLCNAC).

FT CARBOHYD 180 180 REMOVED POST-TRANSLATIONALLY.

FT MOD_RES 330 330 K -> R (IN GIM(3) MARKER).

FT VARIANT 97 97 /FTId=VAR_003886.

FT VARIANT 239 239 D -> E (IN GIM(NON-1) MARKER).

FT VARIANT 239 239 /FTId=VAR_003887.

FT VARIANT 241 241 L -> M (IN GIM(NON-1) MARKER).
 /FTId=VAR_003888.

FT STRAND 123 126 STRAND

FT HELIX 130 134 HELIX

FT TURN 136 137 TURN

FT STRAND 141 148 STRAND

FT STRAND 158 162 STRAND

FT TURN 163 164 TURN

FT STRAND 165 166 STRAND

FT TURN 175 178 TURN

FT STRAND 183 190 STRAND

FT HELIX 193 197 HELIX

FT TURN 198 199 TURN

Query Match 44.8%; Score 1087; DB 1; Length 330;
 Best Local Similarity 60.8%; Pred. No. 7.7e-69; Mismatches 75; Indels 8; Gaps 3;
 Matches 205; Conservative 49; Mismatches 75; Indels 8; Gaps 3;

QY 178 GLYTMSSSVTPPSSTWPSQTVCSVAPASSTVTKLLEPSSGPSTINPOCPCKECHCP 237

Db 61 GLYSLSVSVVTPPSSTGQTVICVNHKPSNTKVVKVPEKSCDT-HTCPP-----CP 113

QY 238 APNLEGGPSVTFPPNPKDVMISLTPKVICVWWDVSEDDPDVQLSWFTVANNVHTAQTO 297

Db 114 APELLGGPSVTFPPNPKDVMISLTPKVICVWWDVSEDDPDVQLSWFTVANNVHTAQTO 173

QY 298 THREDVNSTTRWVSTLPIQHQDWDMSGKEFKKVNKKDLSPIERISKYKGLVRAPOVY 357

Db 174 PREEQONSTVYRVSIVSLVQDWDLNGKEYKVKVSKLPAERIKTSKAKGQPRBQVY 233

QY 358 LPPIPAEQLRSRKDVSEITCLVUGFNPQDLSVETNSGHTEEWYKDTAPVLDSDGSFYISKL 417

Db 234 LPPSDELTLKQVSLCILVKGFPSDIAVENESQOPENYKTPPVLDSDGSFLYSKL 293

QY 418 NMKTSKEWKTDSFSCNVRHEGLKNYLLKKTTSRSRQK 454

Db 294 TVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPCK 330

RESULT 15

GC_RABIT ID GC_RABIT STANDARD; PRT; 323 AA.

AC P01870; DT 21-JUL-1986 (Rel. 01, Created)

AC P01870; DT 21-JUL-1986 (Rel. 01, Last sequence update)

AC P01870; DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG GAMMA CHAIN C REGION.

OS Oryctolagus cuniculus (rabbit). Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI_TaxID=9986; RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=84030930; PubMed=6311520;

RP Bernstein K.E.; Alexander C.B.; Mage R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 RT F-I haplotype.";
 RL Immunogenetics 18:387-397(1983).
 RN [2]

RP SEQUENCE OF 1-128.

RA MEDLINE=76135459; PubMed=1243651;

RT Pratt D.M., Mole L.E.;

RT "Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";

RL Biochem. J. 151:337-349(1975).

[3] RN SEQUENCE OF 88-266 FROM N.A.

RP RX MEDLINE=33299917; PubMed=6193512;

RA Martens C.L., Moore K.W., Steinberg M., Hood L., Knight K.L.;

RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.,"; proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).

[4] RN SEQUENCE OF 132-161.

RP RX MEDLINE=7010015; PubMed=5461106;

RA Fruchtter R.G., Jackson S.A., Mole L.E., Porter R.R.;

RT "Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.,"; Biochem. J. 116:249-259(1970).

[5] RN SEQUENCE OF 129-131 AND 155-322.

RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;

RL (In) Killander J. (eds.);

RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell, Stockholm (1967).

-1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPEIC MARKER, 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15 MARKERS, AND REF.5 THE E15 MARKER.

CC -----

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CC -----

CC EMBL: M16426; AAA31289.1; -.

DR PIR: A02161; GIHRB.

DR InterPro: IPR000495; -.

DR InterPro: IPR003006; -.

DR Pfam: PF00047; 19; 3.

DR PROSITE: PS00280; IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON_TER 1 1

FT VARIANT 104 104 T -> M (IN D11 MARKER).

FT VARIANT 185 185 T -> A (IN E15 MARKER).

FT CONFLICT 48 48 N -> E (IN REF. 2).

FT CONFLICT 71 71 V -> VEV (IN REF. 2).

FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).

FT CONFLICT 173 173 N -> D (IN REF. 5).

FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).

FT CONFLICT 201 201 N -> D (IN REF. 5).

FT CONFLICT 218 218 Q -> E (IN REF. 5).

FT CONFLICT 233 233 E -> Q (IN REF. 5).

FT CONFLICT 246 246 N -> D (IN REF. 5).

FT CONFLICT 256 256 E -> G (IN REF. 5).

FT CONFLICT 260 260 N -> D (IN REF. 5).

FT CONFLICT 266 266 N -> D (IN REF. 5).

FT CONFLICT 280 280 Y -> W (IN REF. 5).

FT CONFLICT 284 284 N -> S (IN REF. 5).

SQ SEQUENCE 323 AA; 35404 MW; 698AA118D579ABB CRC64;

Query Match 44.5%; score 1080.5; DB 1; length 323; Best Local Similarity 61.4%; Pred. No. 2.1e-68; Gaps 19; Matches 205; Conservative 48; Mismatches 62; Indels 19; Gaps 6

QY 124 PSVYPLAPSGCGDTGQSSVTVGLVKGYPESVTWNGSLSSVHFTPALQ-SGLYTM 182

Db 6 PSVYPLAPSGCGDTGQSSVTVGLVKGYPESVTWNGSLSSVHFTPALQ-SGLYTM 65

QY 183 SSSVTPVSPSTWPSQTVTCVSAHPSASSTVDKRLEPSGP1STINPCPPKCECHK--CPAPN 240

Search completed: June 18, 2001, 15:34:34
Job time: 242 sec

Query Match	44.5%	Score 1080.5;	DB 1;	Length 323;
Best Local Similarity	61.48;	Pred. No. 2.1e-68;		
Matches	205; Conservative	48; Mismatches 62;	Indels 19;	Gaps 4;

124 PSSWPLAPGCGBTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLO-SGLYTM 182

183 SSSVTVPSSTPSOTVTCVSAHPASSTVDDKKLEPSCPISTINCPCPCKECHK--CPAPN 240
 6 PSVFLPLAPCCGDTPSSTVTLGCLVKGLPVEPVTVWNNSGTLTNGVRTPSPVROSSGLYSL 65

Tue Jun 19 08:18:09 2001

us-09-653-755a-4.rsp